

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/699,7164DATE: 02/19/97  
TIME: 16:15:59

INPUT SET: S15620.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4 (i) APPLICANT: David G. Heath  
5 Arthur M. Friedlander  
6 George W. Anderson  
7 Susan L. Welkos  
8  
9 (ii) TITLE OF INVENTION: Recombinant F1-V Plague Vaccine  
10  
11 (iii) NUMBER OF SEQUENCES: 6  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: John Moran  
15 (B) STREET: USA MPMC - MPMC-JA  
16 (C) CITY: FORT DETRICK, FREDERICK  
17 (D) STATE: MARYLAND  
18 (E) COUNTRY: USA  
19 (F) ZIP: 21702-5012  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: Apple Macintosh  
24 (C) OPERATING SYSTEM: Macintosh 7.5  
25 (D) SOFTWARE: Microsoft Word 6.0  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER:  
29 (B) FILING DATE:  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER:  
34 (B) FILING DATE:  
35  
36 (viii) ATTORNEY/AGENT INFORMATION:  
37 (A) NAME: Moran, John  
38 (B) REGISTRATION NUMBER: 26,313  
39 (C) REFERENCE/DOCKET NUMBER:  
40  
41 (ix) TELECOMMUNICATION INFORMATION  
42 (A) TELEPHONE: (301) 619-2065  
43 (B) TELEFAX: (301) 619-7714  
44  
45 (2) INFORMATION FOR SEQ ID NO:1:  
46

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/699,716ADATE: 02/19/97  
TIME: 16:16:02

INPUT SET: S15620.raw

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 1566 bp

49 (B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Single

51 (D) TOPOLOGY: Linear

52

53 (ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

54

55 ATGGGCCATC ATCATCATCA TCATCATCAT CATCACAGCA 40

56

57 GCGGCCATAT CGACGACGAC GACAAGCATA TGAAAAAAAT 80

58

59 CAGTTCCGTT ATCGCCATTG CATTATTTGG AACTATTGCA 120

60

61 ACTGCTAATG CGGCAGATTT AACTGCAAGC ACCACTGCAA 160

62

63 CGGCAACTCT TGTTGAACCA GCGCGCATCA CTCTTACATA 200

64

65 TAAGGAAGGC GCTCCAATTA CAATTATGGA CAATGGAAAC 240

66

67 ATCGATACAG AATTACTTGT TGGTACGCTT ACTCTTGGCG 280

68

69 GCTATAAAAC AGGAACCACT AGCACATCTG TTAACCTTAC 320

70

71 AGATGCCGCG GGTGATCCCA TGTACTTAAC ATTTACTTCT 360

72

73 CAGGATGGAA ATAACCACCA ATTCACTACA AAAGTGATTG 400

74

75 GCAAGGATTC TAGAGATTTT GATATCTCTC CTAAGGTAAA 440

76

77 CGGTGAGAAC CTTGTGGGGG ATGACGTCGT CTTGGCTACG 480

78

79 GGCAGCCAGG ATTTCTTTGT TCGCTCAATT GGTTCCAAAG 520

80

81 GCGGTAAACT TGCAGCAGGT AAATACACTG ATGCTGTAAC 560

82

83 CGTAACCGTA TCTAACCAAG AATTCATGAT TAGAGCCTAC 600

84

85 GAACAAAACC CACAACATTT TATTGAGGAT CTAGAAAAAG 640

86

87 TTAGGGTGGA ACAACTTACT GGTCATGGTT CTTCAGTTTT 680

88

89 AGAAGAATTG GTTCAGTTAG TCAAAGATAA AAATATAGAT 720

90

91 ATTTCCATTA AATATGATCC CAGAAAAGAT TCGGAGGTTT 760

92

93 TTGCCAATAG AGTAATTACT GATGATATCG AATTGCTCAA 800

94

95 GAAAATCCTA GCTTATTTTC TACCCGAGGA TACCATTCTT 840

96

97 AAAGGCGGTC ATTATGACAA CCAACTGCAA AATGGCATCA 880

98

99 AGCGAGTAAA AGAGTTCCTT GAATCATCGC CGAATACACA 920

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/699,716A

DATE: 02/19/97  
TIME: 16:16:05

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100
101 ATGGGAATTG CGGGCGTTCA TGGCAGTAAT GCATTTCTCT 960
102
103 TTAACCGCCG ATCGTATCGA TGATGATATT TTGAAAGTGA 1000
104
105 TTGTTGATTC AATGAATCAT CATGGTGATG CCCGTAGCAA 1040
106
107 GTTGCGTGAA GAATTAGCTG AGCTTACCGC CGAATTAAAG 1080
108
109 ATTTATTTCAG TTATTCAAGC CGAAATTAAT AAGCATCTGT 1120
110
111 CTAGTAGTGG CACCATAAAT ATCCATGATA AATCCATTAA 1160
112
113 TCTCATGGAT AAAAATTTAT ATGGTTATAC AGATGAAGAG 1200
114
115 ATTTTAAAG CCAGCGCAGA GTACAAAATT CTCGAGAAAA 1240
116
117 TGCCCTCAAAC CACCATTTCAG GTGGATGGGA GCGAGAAAAA 1280
118
119 AATAGTCTCG ATAAAGGACT TTCTTGGAAG TGAGAATAAA 1320
120
121 AGAACCGGGG CGTTGGGTAA TCTGAAAAAC TCATACTCTT 1360
122
123 ATAATAAAGA TAATAATGAA TTATCTCACT TTGCCACCAC 1400
124
125 CTGCTCGGAT AAGTCCAGGC CGCTCAACGA CTTGGTTAGC 1440
126
127 CAAAAAACAA CTCAGCTGTC TGATATTACA TCACGTTTTA 1480
128
129 ATTCAGCTAT TGAAGCACTG AACCGTTTCA TTCAGAAATA 1520
130
131 TGATTTCAGT ATGCAACGTC TGCTAGATGA CACGTCTGGT 1560
132
133 AAATGA 1566
134
135

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

146 Met Gly His His His His His His His His His His Ser Ser Gly
147 1 5 10 15
148
149 His Ile Asp Asp Asp Asp Lys His Met Lys Lys Ile Ser Ser Val
150 20 25 30
151
152 Ile Ala Ile Ala Leu Phe Gly Thr Ile Ala Thr Ala Asn Ala Ala

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## RAW SEQUENCE LISTING

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153		35		40		45
154						
155	Asp Leu Thr Ala	Ser Thr Thr Ala Thr	Ala Thr Leu Val Glu Pro			
156		50		55		60
157						
158	Ala Arg Ile Thr	Leu Thr Tyr Lys Glu Gly	Ala Pro Ile Thr Ile			
159		65		70		75
160						
161	Met Asp Asn Gly	Asn Ile Asp Thr Glu	Leu Leu Val Gly Thr Leu			
162		80		85		90
163						
164	Thr Leu Gly Gly	Tyr Lys Thr Gly Thr	Thr Ser Thr Ser Val Asn			
165		95		100		105
166						
167	Phe Thr Asp Ala	Ala Gly Asp Pro Met Tyr	Leu Thr Phe Thr Ser			
168		110		115		120
169						
170	Gln Asp Gly Asn	Asn His Gln Phe Thr	Thr Lys Val Ile Gly Lys			
171		125		130		135
172						
173	Asp Ser Arg Asp	Phe Asp Ile Ser Pro	Lys Val Asn Gly Glu Asn			
174		140		145		150
175						
176	Leu Val Gly Asp	Asp Val Val Leu Ala	Thr Gly Ser Gln Asp Phe			
177		155		160		165
178						
179	Phe Val Arg Ser	Ile Gly Ser Lys Gly	Gly Lys Leu Ala Ala Gly			
180		170		175		180
181						
182	Lys Tyr Thr Asp	Ala Val Thr Val Thr	Val Ser Asn Gln Glu Phe			
183		185		190		195
184						
185	Met Ile Arg Ala	Tyr Glu Gln Asn Pro	Gln His Phe Ile Glu Asp			
186		200		205		210
187						
188	Leu Glu Lys Val	Arg Val Glu Gln Leu	Thr Gly His Gly Ser Ser			
189		215		220		225
190						
191	Val Leu Glu Glu	Leu Val Gln Leu Val	Lys Asp Lys Asn Ile Asp			
192		230		235		240
193						
194	Ile Ser Ile Lys	Tyr Asp Pro Arg Lys	Asp Ser Glu Val Phe Ala			
195		245		250		255
196						
197	Asn Arg Val Ile	Thr Asp Asp Ile Glu	Leu Leu Lys Lys Ile Leu			
198		260		265		270
199						
200	Ala Tyr Phe Leu	Pro Glu Asp Thr Ile	Leu Lys Gly Gly His Tyr			
201		275		280		285
202						
203	Asp Asn Gln Leu	Gln Asn Gly Ile Lys	Arg Val Lys Glu Phe Leu			
204		290		295		300
205						

## RAW SEQUENCE LISTING

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206	Glu Ser Ser Pro Asn Thr Gln Trp Glu Leu Arg Ala Phe Met Ala	
207		305 310 315
208		
209	Val Met His Phe Ser Leu Thr Ala Asp Arg Ile Asp Asp Asp Ile	
210		320 325 330
211		
212	Leu Lys Val Ile Val Asp Ser Met Asn His His Gly Asp Ala Arg	
213		335 340 345
214		
215	Ser Lys Leu Arg Glu Glu Leu Ala Glu Leu Thr Ala Glu Leu Lys	
216		350 355 360
217		
218	Ile Tyr Ser Val Ile Gln Ala Glu Ile Asn Lys His Leu Ser Ser	
219		365 370 375
220		
221	Ser Gly Thr Ile Asn Ile His Asp Lys Ser Ile Asn Leu Met Asp	
222		380 385 390
223		
224	Lys Asn Leu Tyr Gly Tyr Thr Asp Glu Glu Ile Phe Lys Ala Ser	
225		395 400 405
226		
227	Ala Glu Tyr Lys Ile Leu Glu Lys Met Pro Gln Thr Thr Ile Gln	
228		410 415 420
229		
230	Val Asp Gly Ser Glu Lys Lys Ile Val Ser Ile Lys Asp Phe Leu	
231		425 430 435
232		
233	Gly Ser Glu Asn Lys Arg Thr Gly Ala Leu Gly Asn Leu Lys Asn	
234		440 445 450
235		
236	Ser Tyr Ser Tyr Asn Lys Asp Asn Asn Glu Leu Ser His Phe Ala	
237		455 460 465
238		
239	Thr Thr Cys Ser Asp Lys Ser Arg Pro Leu Asn Asp Leu Val Ser	
240		470 475 480
241		
242	Gln Lys Thr Thr Gln Leu Ser Asp Ile Thr Ser Arg Phe Asn Ser	
243		485 490 495
244		
245	Ala Ile Glu Ala Leu Asn Arg Phe Ile Gln Lys Tyr Asp Ser Val	
246		500 505 510
247		
248	Met Gln Arg Leu Leu Asp Asp Thr Ser Gly Lys	
249		515 520
250		
251		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bp

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION: US/08/699,716A**

DATE: 02/19/97

TIME: 16:16:16

***INPUT SET: S15620.raw***

Line

Error

Original Text